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Dear Aaron:

Thank you for your letter of 23 June and the Internal memo "Ease of twisting of DNA". Rather than reply at length could you ask Michael Levitt to show you the letter I have just written to him concerning the paper by Camerini-Otero and Felsenfeld. You will see that the whole question of the conformation of superhelical DNA in solution is full of difficulties. For example, are you sure that such DNA is not toroidal at very small |AL|?

I don't think the variation of the sedimentation constant with $|\Delta L|$ is of much use by itself. It's clear we shall need, in addition, the "thermal distribution" of $|\Delta L|$, both around a mean of $|\Delta L|$ wo and also around greater values of $|\Delta L|$. We shall also need the details of the X-ray scattering in solution. On the theoretical side a lot needs to be cleared up. Hopefully a theory will eventually emerge which fits the experimental date in a natural way.

I suggest we leave further discussion till we meet in Denmark. Have you seen the preprint by Sussman and Trifonov? I am sending a copy to Michael just in case he doesn't have one.

I enclose a slightly revised version of the short note for the CSH Symposium. As you will see, it covers a number of points which we have been corresponding about. I feel that is one or two places it is sounder than the account in your paper.

Now about the New Zealand SBS structure. I mention this because you told me one of them would be visiting you in July. There seems to be no definitive papers about D loops but I am told that Kasamatsu et al. PNAS, 68, 2252-2257, 1971 is the main paper. This shows that when you unwind DNA you remove about one turn for every 10 base-pairs and certainly not one turn for every 100 base-pairs. This, by itself, should be enough to dispose of the SBS structure. Mike Botchan and Walter Keller plan to do an improved version of this experiment to see if the base-pairs/turn is nearer 10 1/2 than 10 but this will need much more careful study.

Best wishes,

FHCC/al

F. H. C. Crick